AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently amended). A method for identifying a drug candidate for promoting tissue-specific differentiation of an embryonic stem cell (ES), the method comprising the steps of:

(A) providing a library of test substances~~, the library comprising at least a first test substance and a second test substance, the first and second test substances~~ having different molecular structures;

(B) providing an *in vitro* culture of embryonic stem cells (ES) cultured in hanging drops for 2 days to produce a culture of embryoid bodies, the culture being divided into at least a first subculture and a second subculture and;

(C) culturing the first and second subcultures for at least about 5 days in the absence of a test substance on a ~~collagen coated~~ culture plate coated with collagen or without collagen;

(D) contacting the first subculture with a ~~first~~ test substance and a second subculture with ~~a second~~ another test substance from the library of test substances;

(E) culturing the first and second subcultures for 7 to 18 days; and

(F) analyzing the cells in the first and second subcultures for increased tissue-specific gene expression.

2. (Cancel).

3. (Previously presented) The method of claim 1, wherein the embryonic stem cells are mammalian embryonic stems cells.

4. (Cancel)

5. (Previously presented) The method of claim 1, wherein the embryonic stem cells are murine R1 embryonic stem cells.

6. (Previously presented) The method of claim 1, wherein the embryonic stem cells are human embryonic stem cells.

Claims 7-13. (Cancelled)

14. (Previously Presented) The method of claim 1, wherein the step (F) of analyzing the cells in the first and second subcultures for increased tissue-specific gene expression comprises isolating mRNA from the first and second subcultures.

15. (Original) The method of claim 14, wherein total cellular RNA is isolated from the first and second subcultures.

16. (Previously Presented) The method of claim 14, wherein the step (F) further comprises reverse-transcribing the mRNA to create cDNA.

17. (Previously Presented) The method of claim 1, wherein the step (F) of analyzing the cells in the first and second subcultures for increased tissue-specific gene expression comprises performing a polymerase chain reaction (PCR).

18. (Original) The method of claim 14, wherein the isolated mRNA is immobilized on a substrate.

19. (Original) The method of claim 18, wherein the substrate is contacted with a probe that specifically hybridizes to the tissue-specific mRNA.

20. (Previously Presented) The method of claim 1, wherein the step (F) of analyzing the cells in the first and second subcultures for increased tissue-specific gene expression is performed using gene chip technology.